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aatattaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 878

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<211> 145

<212> PRT

<213> Homo sapiens

<400> 27

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Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly Cys His Cys
15 20 25

Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr Asp Trp Cys Cys
30 35 40

Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys Thr Gln Gly Cys Gly
45 50 55 60

Ile Tyr Lys Asp Tyr Tyr Arg Tyr Asn Phe Ser Gln Gly Asn Ile His
65 70 75

Cys Ser Asp Lys Gly Ser Trp Cys Glu Gln Gln Leu Cys Ala Cys Asp
80 85 90

Lys Glu Val Ala Phe Cys Leu Lys Arg Asn Leu Asp Thr Tyr Gln Lys
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Cys
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- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | | | | DB | ID | Description |
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| | Score | Match | Length | % | | | |
| 1 | 852 | 100.0 | 145 | 4 | US-09-856-486-27 | Sequence 27, Appl | |
| 2 | 624.5 | 73.3 | 144 | 4 | US-09-856-486-14 | Sequence 14, Appl | |
| 3 | 500.5 | 58.7 | 116 | 4 | US-10-140-002-534 | Sequence 534, App | |
| 4 | 401.5 | 47.1 | 146 | 3 | US-08-966-317-4 | Sequence 4, Appli | |
| 5 | 401.5 | 47.1 | 146 | 3 | US-09-489-770-4 | Sequence 4, Appli | |
| 6 | 400.5 | 47.0 | 146 | 2 | US-08-888-497-35 | Sequence 35, Appl | |
| 7 | 400.5 | 47.0 | 146 | 3 | US-09-362-230-35 | Sequence 35, Appl | |
| 8 | 400.5 | 47.0 | 146 | 5 | PCT-US94-07926-35 | Sequence 35, Appl | |
| 9 | 395.5 | 46.4 | 144 | 1 | US-08-186-895-10 | Sequence 10, Appl | |
| 10 | 395.5 | 46.4 | 144 | 2 | US-08-888-497-37 | Sequence 37, Appl | |
| 11 | 395.5 | 46.4 | 144 | 3 | US-09-362-230-37 | Sequence 37, Appl | |
| 12 | 395.5 | 46.4 | 144 | 5 | PCT-US94-07926-37 | Sequence 37, Appl | |
| 13 | 371.5 | 43.6 | 146 | 3 | US-08-966-317-3 | Sequence 3, Appli | |

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 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|--------|--------------------|
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| 2 | 399.5 | 46.9 | 146 | 2 | A33394 | phospholipase A2 (|
| 3 | 395.5 | 46.4 | 144 | 1 | PSHUYF | phospholipase A2 (|
| 4 | 389.5 | 45.7 | 146 | 2 | JU0283 | phospholipase A2 (|
| 5 | 389 | 45.7 | 145 | 2 | I48093 | phospholipase A2 (|
| 6 | 365.5 | 42.9 | 146 | 2 | I48342 | phospholipase A2 (|
| 7 | 347 | 40.7 | 138 | 2 | A49959 | phospholipase A2 (|
| 8 | 335.5 | 39.4 | 138 | 1 | I51381 | phospholipase A2 (|
| 9 | 335.5 | 39.4 | 138 | 1 | PSRSBT | phospholipase A2 (|
| 10 | 332 | 39.0 | 125 | 2 | JX0052 | phospholipase A2 (|
| 11 | 331.5 | 38.9 | 138 | 1 | PSRSB2 | phospholipase A2 (|
| 12 | 328.5 | 38.6 | 138 | 2 | JC1342 | phospholipase A2 (|
| 13 | 320.5 | 37.6 | 122 | 2 | S13900 | phospholipase A2 (|
| 14 | 319.5 | 37.5 | 137 | 2 | S68429 | myotoxin precursor |
| 15 | 316.5 | 37.1 | 122 | 1 | PSTVXF | phospholipase A2 (|
| 16 | 314.5 | 36.9 | 138 | 2 | S10992 | ammodytin L precur |

Database : UniProt_02:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 624.5 | 73.3 | 144 | 1 | PA2D_MOUSE | Q9wvf6 mus musculu |
| 3 | 500.5 | 58.7 | 116 | 2 | Q6UWX0 | Q6uwx0 homo sapien |
| 4 | 500.5 | 58.7 | 116 | 2 | AAQ88969 | Aaq88969 homo sapi |
| 5 | 400.5 | 47.0 | 146 | 2 | Q91Y34 | Q91y34 rattus norv |
| 6 | 399.5 | 46.9 | 146 | 1 | PA2A_RAT | P14423 rattus norv |
| 7 | 395.5 | 46.4 | 144 | 1 | PA2A_HUMAN | P14555 homo sapien |
| 8 | 395.5 | 46.4 | 144 | 2 | CAG33146 | Cag33146 homo sapi |
| 9 | 393.5 | 46.2 | 144 | 2 | Q6DN24 | Q6dn24 homo sapien |

RESULT 1

PA2D_HUMAN

ID PA2D_HUMAN STANDARD; PRT; 145 AA.
AC Q9UNK4; Q9UK01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase GIID) (GIID sPLA2) (PLA2IID)
DE (sPLA(2)-IID) (Secretory-type PLA, stroma-associated homolog).
GN Name=PLA2G2D; Synonyms=SPLASH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., VARIANT GLY-80, AND CHARACTERIZATION.
RX MEDLINE=99386983; PubMed=10455175;
RA Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,
RA Kawamoto K., Fujii N., Arita H., Hanasaki K.;
RT "Cloning and characterization of novel mouse and human secretory
RT phospholipase A2s.";
RL J. Biol. Chem. 274:24973-24979(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21040292; PubMed=11196711; DOI=10.1038/sj.gene.6363659;
RA Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,
RA Nedospasov S.A.;
RT "SPLASH (PLA(2)IID), a novel member of phospholipase A2 family, is
RT associated with lymphotoxin-deficiency.";
RL Genes Immun. 1:191-199(2000).
RN [3]
RP SEQUENCE FROM N.A.
RA Wallis J.;
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
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RC TISSUE=Pancreas, and Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitoyl-2-linoleoyl phosphatidylethanolamine is more efficiently hydrolyzed than the other phospholipids examined.

CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.

CC -!- COFACTOR: Binds 1 calcium ion per subunit.

CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

CC -!- TISSUE SPECIFICITY: Broadly expressed.

CC -!- MISCELLANEOUS: Maximally active at neutral to alkaline pH and with 2 mM Ca(2+).

CC -!- SIMILARITY: Belongs to the phospholipase A2 family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; AF112982; AAD51390.1; -.

DR EMBL; AF188625; AAF09020.1; -.

DR EMBL; AL158172; CAC13159.1; -.

DR EMBL; BC025706; AAH25706.1; -.

DR HSSP; P14555; 1POD.

DR Genew; HGNC:9033; PLA2G2D.

DR MIM; 605630; -.

DR GO; GO:0005576; C:extracellular; TAS.

DR GO; GO:0004623; F:phospholipase A2 activity; TAS.

DR GO; GO:0006954; P:inflammatory response; TAS.

DR GO; GO:0006644; P:phospholipid metabolism; TAS.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phospholip_A2_1; 1.

DR PRINTS; PR00389; PHPHLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2_ASP; 1.

DR PROSITE; PS00118; PA2_HIS; 1.

KW Calcium; Hydrolase; Lipid degradation; Polymorphism; Signal.

| | | | | |
|----|----------|-----|-----|--|
| FT | SIGNAL | 1 | 20 | Potential. |
| FT | CHAIN | 21 | 145 | Group IID secretory phospholipase A2. |
| FT | ACT_SITE | 67 | 67 | By similarity. |
| FT | ACT_SITE | 112 | 112 | By similarity. |
| FT | DISULFID | 46 | 138 | By similarity. |
| FT | DISULFID | 48 | 64 | By similarity. |
| FT | DISULFID | 63 | 118 | By similarity. |
| FT | DISULFID | 69 | 145 | By similarity. |
| FT | DISULFID | 70 | 111 | By similarity. |
| FT | DISULFID | 79 | 104 | By similarity. |
| FT | DISULFID | 97 | 109 | By similarity. |
| FT | CARBOHYD | 89 | 89 | N-linked (GlcNAc . . .) (Potential). |
| FT | METAL | 47 | 47 | Calcium (via carbonyl oxygen) (By similarity). |
| FT | METAL | 49 | 49 | Calcium (via carbonyl oxygen) (By |

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 Db 1 MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDAT 60
 QY 61 DWCCQTHDCCYDHLKTQGCGIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 DWCCQTHDCCYDHLKTQGCSIYKDYRYNFSQGNIHCSDKGSWCEQQLCACDKEVAFCLK 120
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- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| No. | Score | Match | Length | DB | ID | | | | | |
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| 2 | 843 | 96.0 | 1937 | 6 | CQ726642 | | | | | CQ726642 Sequence |
| 3 | 832 | 94.8 | 2747 | 9 | BC025706 | | | | | BC025706 Homo sapi |
| 4 | 831 | 94.6 | 1938 | 9 | AF188625 | | | | | AF188625 Homo sapi |
| c 5 | 524.6 | 59.7 | 98743 | 9 | AL158172 | | | | | AL158172 Human DNA |
| 6 | 296 | 33.7 | 1233 | 6 | E37214 | | | | | E37214 Mouse secre |
| 7 | 296 | 33.7 | 1233 | 10 | AF112983 | | | | | AF112983 Mus muscu |
| 8 | 296 | 33.7 | 1975 | 10 | AF169407 | | | | | AF169407 Mus muscu |
| 9 | 296 | 33.7 | 2166 | 10 | AF169408 | | | | | AF169408 Mus muscu |
| 10 | 284.2 | 32.4 | 496 | 6 | AX464400 | | | | | AX464400 Sequence |
| 11 | 284.2 | 32.4 | 496 | 6 | AX697309 | | | | | AX697309 Sequence |

RESULT 1
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DEFINITION Homo sapiens group IID secretory phospholipase A2 (PLA2) mRNA,
complete cds.
ACCESSION AF112982
VERSION AF112982.1 GI:5771419
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS Ishizaki,J., Suzuki,N., Higashino,K., Yokota,Y., Ono,T.,
Kawamoto,K., Fujii,N., Arita,H. and Hanasaki,K.
TITLE Cloning and characterization of novel mouse and human secretory
phospholipase A(2)s
JOURNAL J. Biol. Chem. 274 (35), 24973-24979 (1999)
MEDLINE 99386983
PUBMED 10455175
REFERENCE 2 (bases 1 to 878)
AUTHORS Ishizaki,J., Suzuki,N., Higashino,K. and Hanasaki,K.
TITLE Direct Submission
JOURNAL Submitted (11-DEC-1998) Shionogi Research Laboratories,
Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
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/note="results in glycine to serine substitution"
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ORIGIN

Query Match 100.0%; Score 878; DB 9; Length 878;
Best Local Similarity 100.0%; Pred. No. 4.6e-215;
Matches 878; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAAGCTTGCAGTCTGTGTGGGCTGGTGGT 60
|||||
Db 1 TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAAGCTTGCAGTCTGTGTGGGCTGGTGGT 60
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[illegible]

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- 12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | % | | Query | | DB | ID | Description |
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| | No. | Score | Match | Length | | | | | |
| c | 1 | 878 | 100.0 | 878 | 3 | AAA60878 | | Aaa60878 | Human sec |
| | 2 | 843 | 96.0 | 2789 | 12 | ADQ22737 | | Adq22737 | Human sof |
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| | 4 | 832 | 94.8 | 2747 | 10 | ACC72857 | | Acc72857 | Human can |
| | 5 | 831 | 94.6 | 1938 | 12 | ADQ18176 | | Adq18176 | Human sof |
| | 6 | 830 | 94.5 | 854 | 4 | AAS14884 | | Aas14884 | Human cDN |
| | 7 | 821.4 | 93.6 | 1927 | 4 | AAH98759 | | Aah98759 | Human EST |
| | 8 | 821.4 | 93.6 | 1927 | 4 | AAH99768 | | Aah99768 | Human pro |
| | 9 | 820 | 93.4 | 1931 | 5 | AAD19218 | | Aad19218 | Human CG9 |
| | 10 | 592 | 67.4 | 592 | 3 | AAA53269 | | Aaa53269 | Human pho |
| | 11 | 518.2 | 59.0 | 577 | 12 | ACH76501 | | Ach76501 | Human gen |
| | 12 | 296 | 33.7 | 1233 | 3 | AAA60866 | | Aaa60866 | Mouse sec |
| | 13 | 296 | 33.7 | 1233 | 3 | AAA72076 | | Aaa72076 | cDNA enco |
| | 14 | 284.2 | 32.4 | 496 | 3 | AAA77684 | | Aaa77684 | Human PRO |

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % | | DB | ID | Description |
|---------------|-------|-------|--------------|----|--------------------|-------------------|
| | | Query | Match Length | | | |
| 1 | 878 | 100.0 | 878 | 4 | US-09-856-486-26 | Sequence 26, Appl |
| 2 | 296 | 33.7 | 1233 | 4 | US-09-856-486-13 | Sequence 13, Appl |
| 3 | 284.2 | 32.4 | 496 | 4 | US-10-140-002-533 | Sequence 533, App |
| 4 | 268.8 | 30.6 | 501 | 4 | US-09-856-486-1 | Sequence 1, Appli |
| 5 | 119.6 | 13.6 | 1016 | 4 | US-09-220-132-17 | Sequence 17, Appl |
| 6 | 118 | 13.4 | 1014 | 2 | US-08-888-497-31 | Sequence 31, Appl |
| 7 | 118 | 13.4 | 1014 | 3 | US-09-362-230-31 | Sequence 31, Appl |
| 8 | 118 | 13.4 | 1014 | 5 | PCT-US94-07926-31 | Sequence 31, Appl |
| 9 | 112.4 | 12.8 | 479 | 1 | US-08-186-895-9 | Sequence 9, Appli |
| 10 | 110.8 | 12.6 | 854 | 4 | US-09-023-655-1207 | Sequence 1207, Ap |
| 11 | 101.8 | 11.6 | 375 | 4 | US-09-740-569-1 | Sequence 1, Appli |
| 12 | 101.8 | 11.6 | 375 | 4 | US-10-255-576-1 | Sequence 1, Appli |
| 13 | 98.4 | 11.2 | 1828 | 2 | US-08-888-497-29 | Sequence 29, Appl |
| 14 | 98.4 | 11.2 | 1828 | 3 | US-09-362-230-29 | Sequence 29, Appl |

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- 1: gb_est1:*
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- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | | % | | Query | | DB | ID | Description |
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| | No. | Score | Match | Length | Match | Length | | | |
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| | 2 | 600.2 | 68.4 | 680 | 4 | BI836812 | | BI836812 | 603084703 |
| | 3 | 436.4 | 49.7 | 438 | 9 | AY417051 | | AY417051 | Homo sapi |
| | 4 | 436.4 | 49.7 | 438 | 9 | AY417052 | | AY417052 | Pan trogl |
| | 5 | 427.2 | 48.7 | 463 | 4 | BM153087 | | BM153087 | TCBAP1Q13 |
| | 6 | 342.4 | 39.0 | 631 | 9 | AG079586 | | AG079586 | Pan trogl |
| c | 7 | 323 | 36.8 | 461 | 6 | CB481980 | | CB481980 | jns85_C09 |
| | 8 | 308.6 | 35.1 | 424 | 6 | CD687559 | | CD687559 | EST4080 h |
| | 9 | 296.6 | 33.8 | 623 | 6 | BY752231 | | BY752231 | BY752231 |
| | 10 | 296 | 33.7 | 770 | 7 | CK478998 | | CK478998 | AGENCOURT |
| | 11 | 296 | 33.7 | 1582 | 3 | AK018005 | | AK018005 | Mus muscu |
| | 12 | 291 | 33.1 | 794 | 7 | CK476867 | | CK476867 | AGENCOURT |
| | 13 | 289.8 | 33.0 | 438 | 9 | AY417053 | | AY417053 | Mus muscu |
| | 14 | 268.8 | 30.6 | 460 | 1 | AI430241 | | AI430241 | vv49h02.y |
| | 15 | 268.8 | 30.6 | 501 | 1 | AA762051 | | AA762051 | vv49h02.r |

Database : A_Geneseq_23Sep04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|---------------|-------|------------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 852 | 100.0 | 145 | 3 | AAB03627 | Aab03627 Human pho |
| 2 | 852 | 100.0 | 145 | 3 | AAB12537 | Aab12537 Human sec |
| 3 | 852 | 100.0 | 145 | 4 | AAM24100 | Aam24100 Human EST |
| 4 | 852 | 100.0 | 145 | 4 | AAE11924 | Aae11924 Human CG9 |
| 5 | 852 | 100.0 | 145 | 8 | ADP18678 | Adp18678 Human pro |
| 6 | 852 | 100.0 | 150 | 4 | AAM25827 | Aam25827 Human pro |
| 7 | 846 | 99.3 | 145 | 4 | AAU09096 | Aau09096 Novel hum |
| 8 | 846 | 99.3 | 145 | 6 | ABR44234 | Abr44234 Human sec |
| 9 | 846 | 99.3 | 145 | 6 | ABR58706 | Abr58706 Human can |
| 10 | 846 | 99.3 | 145 | 6 | ABU63124 | Abu63124 Human gro |
| 11 | 846 | 99.3 | 145 | 8 | ADQ18177 | Adq18177 Human sof |
| 12 | 624.5 | 73.3 | 144 | 3 | AAB12536 | Aab12536 Mouse sec |
| 13 | 624.5 | 73.3 | 144 | 3 | AAB11994 | Aab11994 Mouse sec |
| 14 | 500.5 | 58.7 | 116 | 3 | AAB24434 | Aab24434 Human PRO |
| 15 | 500.5 | 58.7 | 116 | 3 | AAY99450 | Aay99450 Human PRO |
| 16 | 500.5 | 58.7 | 116 | 4 | AAB66199 | Aab66199 Protein o |